

# SEQUENCE LISTING

<110> Sacktor, Todd C.

<120> A MEMORY ENHANCING PROTEIN

<130> The Research Foundation Albany

<140> 09/839,073

<141> 2001-04-20

<160> 4

<170> PatentIn Ver. 2.1

<210> 1

<211> 2058

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (444)..(1670)

<220>

<221> unsure

<222> (522)

<223> r at position 522 is g or a

<400> 1

```

cccgggcctg gagacatgag gaggcagggg tgtgaggggc gggggacagg acagccggcc 60
ttccgttaaa tatctgctcc tcgcgctcga gcctccctgc ctattgtcgg ggccggagcg 120
aagccgacgc agcatcagct cgtcaacggg aaggaagatg cctccctgca cgcccgccgc 180
gcacagagca taaagaatct gcgctgagga ggcaggagaa gaaagccgaa tctatctacc 240
gccgggggagc cagaagatgg aggaagctgt accgtgccaa cggccacctc ttccaagcca 300
agcgctttaa caggagagcg tactgcggtc agtgcagcga gaggatatgg ggcctcgcga 360
ggcaaggcta caggtgcatc aactgcaaac tgctggtcca taagcgctgc cacggcctcg 420
tcccgctgac ctgcaggaag cat atg gat tct gtc atg cct tcc caa gag cct 473
                        Met Asp Ser Val Met Pro Ser Gln Glu Pro
                        1                      5                      10

cca gta gac gac aag aac gag gac gcc gac ctt cct tcc gag gag aca 521
Pro Val Asp Asp Lys Asn Glu Asp Ala Asp Leu Pro Ser Glu Glu Thr
                        15                      20                      25

rat gga att gct tac att tcc tca tcc cgg aag cat gac agc att aaa 569
Xaa Gly Ile Ala Tyr Ile Ser Ser Ser Arg Lys His Asp Ser Ile Lys
                        30                      35                      40

gac gac tcg gag gac ctt aag cca gtt atc gat ggg atg gat gga atc 617
Asp Asp Ser Glu Asp Leu Lys Pro Val Ile Asp Gly Met Asp Gly Ile
                        45                      50                      55

aaa atc tct cag ggg ctt ggg ctg cag gac ttt gac cta atc aga gtc 665
Lys Ile Ser Gln Gly Leu Gly Leu Gln Asp Phe Asp Leu Ile Arg Val
                        60                      65                      70

```

atc Ile 75	ggg Gly	cgc Arg	ggg Gly	agc Ser	tac Tyr 80	gcc Ala	aag Lys	gtt Val	ctc Leu	ctg Leu 85	gtg Val	cgg Arg	ttg Leu	aag Lys	aag Lys 90	713
aat Asn	gac Asp	caa Gln	att Ile	tac Tyr 95	gcc Ala	atg Met	aaa Lys	gtg Val	gtg Val 100	aag Lys	aaa Lys	gag Glu	ctg Leu	gtg Val 105	cat His	761
gat Asp	gac Asp	gag Glu	gat Asp 110	att Ile	gac Asp	tgg Trp	gta Val	cag Gln 115	aca Thr	gag Glu	aag Lys	cac His	gtg Val 120	ttt Phe	gag Glu	809
cag Gln	gca Ala	tcc Ser 125	agc Ser	aac Asn	ccc Pro	ttc Phe	ctg Leu 130	gtc Val	gga Gly	tta Leu	cac His	tcc Ser 135	tgc Cys	ttc Phe	cag Gln	857
acg Thr	aca Thr 140	agt Ser	cgg Arg	ttg Leu	ttc Phe	ctg Leu 145	gtc Val	att Ile	gag Glu	tac Tyr	gtc Val 150	aac Asn	ggc Gly	ggg Gly	gac Asp	905
ctg Leu 155	atg Met	ttc Phe	cac His	atg Met	cag Gln 160	agg Arg	cag Gln	agg Arg	aag Lys	ctc Leu 165	cct Pro	gag Glu	gag Glu	cac His	gcc Ala 170	953
agg Arg	ttc Phe	tac Tyr	gcg Ala	gcc Ala 175	gag Glu	atc Ile	tgc Cys	atc Ile	gcc Ala 180	ctc Leu	aac Asn	ttc Phe	ctg Leu	cac His 185	gag Glu	1001
agg Arg	ggg Gly	atc Ile	atc Ile 190	tac Tyr	agg Arg	gac Asp	ctg Leu	aag Lys 195	ctg Leu	gac Asp	aac Asn	gtc Val	ctc Leu 200	ctg Leu	gat Asp	1049
gcg Ala	gac Asp	ggg Gly 205	cac His	atc Ile	aag Lys	ctc Leu	aca Thr 210	gac Asp	tac Tyr	ggc Gly	atg Met	tgc Cys 215	aag Lys	gaa Glu	ggc Gly	1097
ctg Leu	ggc Gly 220	cct Pro	ggt Gly	gac Asp	aca Thr	acg Thr 225	agc Ser	act Thr	ttc Phe	tgc Cys	gga Gly 230	acc Thr	ccg Pro	aat Asn	tac Tyr	1145
atc Ile 235	gcc Ala	ccc Pro	gaa Glu	atc Ile	ctg Leu 240	cgg Arg	gga Gly	gag Glu	gag Glu	tac Tyr 245	ggg Gly	ttc Phe	agc Ser	gtg Val	gac Asp 250	1193
tgg Trp	tgg Trp	gcg Ala	ctg Leu	gga Gly 255	gtc Val	ctc Leu	atg Met	ttt Phe	gag Glu 260	atg Met	atg Met	gcc Ala	ggg Gly	cgc Arg 265	tcc Ser	1241
ccg Pro	ttc Phe	gac Asp	atc Ile 270	atc Ile	acc Thr	gac Asp	aac Asn	ccg Pro 275	gac Asp	atg Met	aac Asn	aca Thr	gag Glu 280	gac Asp	tac Tyr	1289
ctt Leu	ttc Phe	caa Gln 285	gtg Val	atc Ile	ctg Leu	gag Glu	aag Lys 290	ccc Pro	atc Ile	cgg Arg	atc Ile	ccc Pro 295	cgg Arg	ttc Phe	ctg Leu	1337
tcc Ser	gtc Val 300	aaa Lys	gcc Ala	tcc Ser	cat His	gtt Val 305	tta Leu	aaa Lys	gga Gly	ttt Phe 310	tta Leu	aat Asn	aag Lys	gac Asp	ccc Pro	1385
aaa Lys 315	gag Glu	agg Arg	ctc Leu	ggc Gly	tgc Cys 320	cgg Arg	cca Pro	cag Gln	act Thr	gga Gly 325	ttt Phe	tct Ser	gac Asp	atc Ile	aag Lys 330	1433

tcc cac gcg ttc ttc cgc agc ata gac tgg gac ttg ctg gag aag aag 1481  
 Ser His Ala Phe Phe Arg Ser Ile Asp Trp Asp Leu Leu Glu Lys Lys  
 335 340 345  
 cag gcg ctc cct cca ttc cag cca cag atc aca gac gac tac ggt ctg 1529  
 Gln Ala Leu Pro Pro Phe Gln Pro Gln Ile Thr Asp Asp Tyr Gly Leu  
 350 355 360  
 gac aac ttt gac aca cag ttc acc agc gag ccc gtg cag ctg acc cca 1577  
 Asp Asn Phe Asp Thr Gln Phe Thr Ser Glu Pro Val Gln Leu Thr Pro  
 365 370 375  
 gac gat gag gat gcc ata aag agg atc gac cag tca gag ttc gaa ggc 1625  
 Asp Asp Glu Asp Ala Ile Lys Arg Ile Asp Gln Ser Glu Phe Glu Gly  
 380 385 390  
 ttt gag tat atc aac cca tta ttg ctg tcc acc gag gag tcg gtg 1670  
 Phe Glu Tyr Ile Asn Pro Leu Leu Leu Ser Thr Glu Glu Ser Val  
 395 400 405  
 tgaggccgcg tgcgtctctg tcgtggacac gcgtgattga ccccttaact gtatccttaa 1730  
 ccaccgcata tgcatgccag gctgggcacg gctccgaggg cggccagggg cagacgcttg 1790  
 cgccgagacc gcagagggaa gcgtcagcgg gcgctgctgg gagcagaaca gtccctcaca 1850  
 cctggcccgg caggcagctt cgtgctggag gaacttgctg ctgtgcctgc gtcgcggcgg 1910  
 atccgcgggg accctgccga gggggctgtc atgcggtttc caaggtgcac attttccacg 1970  
 gaaacagaac tcgatgcact gacctgtctc gccaggaaag tgagcgtgta gcgtcctgag 2030  
 gaataaaatg ttccgatgaa aaaaaaaa 2058

<210> 2  
 <211> 409  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> (27)  
 <223> Xaa at position 27 is Asp or Asn

<400> 2  
 Met Asp Ser Val Met Pro Ser Gln Glu Pro Pro Val Asp Asp Lys Asn  
 1 5 10 15  
 Glu Asp Ala Asp Leu Pro Ser Glu Glu Thr Xaa Gly Ile Ala Tyr Ile  
 20 25 30  
 Ser Ser Ser Arg Lys His Asp Ser Ile Lys Asp Asp Ser Glu Asp Leu  
 35 40 45  
 Lys Pro Val Ile Asp Gly Met Asp Gly Ile Lys Ile Ser Gln Gly Leu  
 50 55 60  
 Gly Leu Gln Asp Phe Asp Leu Ile Arg Val Ile Gly Arg Gly Ser Tyr  
 65 70 75 80  
 Ala Lys Val Leu Leu Val Arg Leu Lys Lys Asn Asp Gln Ile Tyr Ala  
 85 90 95

Met Lys Val Val Lys Lys Glu Leu Val His Asp Asp Glu Asp Ile Asp  
 100 105 110  
 Trp Val Gln Thr Glu Lys His Val Phe Glu Gln Ala Ser Ser Asn Pro  
 115 120 125  
 Phe Leu Val Gly Leu His Ser Cys Phe Gln Thr Thr Ser Arg Leu Phe  
 130 135 140  
 Leu Val Ile Glu Tyr Val Asn Gly Gly Asp Leu Met Phe His Met Gln  
 145 150 155 160  
 Arg Gln Arg Lys Leu Pro Glu Glu His Ala Arg Phe Tyr Ala Ala Glu  
 165 170 175  
 Ile Cys Ile Ala Leu Asn Phe Leu His Glu Arg Gly Ile Ile Tyr Arg  
 180 185 190  
 Asp Leu Lys Leu Asp Asn Val Leu Leu Asp Ala Asp Gly His Ile Lys  
 195 200 205  
 Leu Thr Asp Tyr Gly Met Cys Lys Glu Gly Leu Gly Pro Gly Asp Thr  
 210 215 220  
 Thr Ser Thr Phe Cys Gly Thr Pro Asn Tyr Ile Ala Pro Glu Ile Leu  
 225 230 235 240  
 Arg Gly Glu Glu Tyr Gly Phe Ser Val Asp Trp Trp Ala Leu Gly Val  
 245 250 255  
 Leu Met Phe Glu Met Met Ala Gly Arg Ser Pro Phe Asp Ile Ile Thr  
 260 265 270  
 Asp Asn Pro Asp Met Asn Thr Glu Asp Tyr Leu Phe Gln Val Ile Leu  
 275 280 285  
 Glu Lys Pro Ile Arg Ile Pro Arg Phe Leu Ser Val Lys Ala Ser His  
 290 295 300  
 Val Leu Lys Gly Phe Leu Asn Lys Asp Pro Lys Glu Arg Leu Gly Cys  
 305 310 315 320  
 Arg Pro Gln Thr Gly Phe Ser Asp Ile Lys Ser His Ala Phe Phe Arg  
 325 330 335  
 Ser Ile Asp Trp Asp Leu Leu Glu Lys Lys Gln Ala Leu Pro Pro Phe  
 340 345 350  
 Gln Pro Gln Ile Thr Asp Asp Tyr Gly Leu Asp Asn Phe Asp Thr Gln  
 355 360 365  
 Phe Thr Ser Glu Pro Val Gln Leu Thr Pro Asp Asp Glu Asp Ala Ile  
 370 375 380  
 Lys Arg Ile Asp Gln Ser Glu Phe Glu Gly Phe Glu Tyr Ile Asn Pro  
 385 390 395 400  
 Leu Leu Leu Ser Thr Glu Glu Ser Val  
 405

<210> 3  
 <211> 2058

<212> DNA  
<213> Homo sapiens

<400> 3

```
gggcccggac ctctgtactc ctccgtccct acactccccg cccctgtgcc tgtcggccgg 60
aaggcaatth atagacgagg agcgcgagct cggagggacg gataacagcc ccggcctcgc 120
ttcggctgcg tcgtagtcga gcagttgcc ttctttctac ggagggacgt gcgggcggcg 180
cgtgtctcgt atttcttaga cgcgactcct ccgtcctctt ctttcggctt agatagatgg 240
cggccccctc gtctttctacc tctttcgaca tggcacgggt gccggtggag aagggttcgg 300
tcgcgaaatt gtcctctcgc atgacgccag tcacgtcgct ctctatacc ccggagcgct 360
ccgttccgat gtccacgtag ttgacgtttg acgaccagggt attcgcgacg gtgccggagc 420
agggcgactg gacgtccttc gtatacctaa gacagtacgg aagggttctc ggagggtcatc 480
tgctgttctt gtcctgcgg gctcctgcg ggctcctctg tctaccttaa cgaatgtaaa 540
ggagtagggc cttcgtactg tcgtaatttc tgctgagcct cctggaattc ggtcaatagc 600
taccctacct accttagttt tagagagtcc ccgaaccga cgtcctgaaa ctggattagt 660
ctcagtagcc cgcgccctcg atgcggttcc aagaggacca cgccaaactt ttcttactgg 720
tttaaagtgc gtactttcac cacttctttc tcgaccacgt actactgctc ctataactga 780
cccatgtctg tctcttcgtg cacaactcgc tccgtagggt gttggggaag gaccagccta 840
atgtgaggac gaaggctcgc tgttcagcca acaaggacca gtaactcatg cagttgccgc 900
ccctggacta caaggtgtac gtctccgtct ccttcgaggg actcctcgtg cgggtccaaga 960
tgcgccggct ctagacgtag cgggagttga aggacgtgct ctccccctag tagatgtccc 1020
tggacttcga cctgttgcag gaggacctac gcctgcccgt gtagttcgag tgtctgatgc 1080
cgtacacgtt ctttccggac ccgggaccac tgtgttgctc gtgaaagacg ccttggggct 1140
taatgtagcg ggggctttag gacgccccct tcctcatgcc caagtcgcac ctgaccacc 1200
gcgaccctca ggagtacaaa ctctactacc ggccgcgcag gggcaagctg tagtagtggc 1260
tgttggcctt gtacttgtgt ctctgatgg aaaaggttca ctaggacctc ttcgggtagg 1320
cctagggggc caaggacagg cagtttcgga gggtaaaaa ttttctaaa aatttattcc 1380
tggggtttct ctccgagccg acggccgggt tctgacctaa aagactgtag ttcagggtgc 1440
gcaagaaggc gtcgtatctg accctgaacg acctcttctt cgtccgcgag ggaggtaagg 1500
tcggtgtcta gtgtctgctg atgccagacc tgttgaaact gtgtgtcaag tggtcgctcg 1560
ggcacgtcga ctggggctcg ctactcctac ggtatttctc ctagtgtgtc agtctcaagc 1620
ttccgaaact catatagttg ggtaataacg acagggtggc cctcagccac actccggcgc 1680
acgcagagac agcacctgtg cgcactaact gggaaattga cataggaatt ggtggcgat 1740
acgtacggtc cgaccctgct cgaggctccc gccggtccct gtctgcgaac gcggctctgg 1800

cgtctccctt cgcagtcgcc cgcgacgacc ctctctttgt cagggagtgt ggaccgggcc 1860
gtccgtcgaa gcacgacctc cttgaacgac gacacggacg cagcgccgcc taggcgcccc 1920
tgggacggct ccccgacag tacgccaaag gttccacgtg taaaagggtc ctttgtcttg 1980
agctacgtga ctggacgagg cggctctttc actcgacat cgcaggactc cttattttac 2040
aaggctactt tttttttt 2058
```

<210> 4  
<211> 13  
<212> PRT  
<213> Unknown Organism

<220>  
<223> Description of Unknown Organism: mzip peptide

<400> 4

```
Ser Ile Tyr Arg Arg Gly Ala Arg Arg Trp Arg Lys Leu
 1           5           10
```